

GenCore version 5.1.4 p5.4578
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OM protein - protein search, using sw model

Run on: March 17, 2003, 08:49:19 ; Search time 159 Seconds
(without alignments)
3154.732 Million cell updates/sec

Title: US-10-010-227-3
Perfect score: 4055
Sequence: 1 MPQAEPTQTLXDKVLQAHV.....KAVPVTNRGEEKPELEW 778

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues
Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

Pending Patents_AA Main:*

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27: /cgn2_6/ptodata/2/paa/US60_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4055	100.0	778	24	US-10-010-227-3
2	3397	83.8	840	27	US-60-360-039-1233
3	2456.5	60.6	779	27	US-60-360-039-11952
4	2451.5	60.5	794	25	US-10-179-131-8614
5	2076	51.2	644	21	US-09-791-537-121852
6	2068.5	51.0	875	27	US-60-360-039-7864

7	2055	50.7	695	27	US-60-360-039-9965	Sequence 9965, Ap
8	2018.5	49.0	710	27	US-60-360-039-15849	Sequence 15849, A
9	1995	48.2	752	27	US-60-360-039-15479	Sequence 15479, A
10	1978	48.8	755	27	US-60-360-039-9413	Sequence 9413, Ap
11	1978	48.4	749	27	US-60-360-039-17883	Sequence 17883, A
12	1953.5	48.2	681	27	US-60-360-039-9308	Sequence 9308, Ap
13	1955.5	48.2	681	27	US-60-360-039-8616	Sequence 8616, Ap
14	1891	46.4	740	27	US-60-360-039-7437	Sequence 7437, Ap
15	1881	46.4	729	27	US-60-360-039-4678	Sequence 4678, Ap
16	1861	45.9	686	27	US-60-360-039-7055	Sequence 7055, Ap
17	1857	45.8	688	27	US-60-360-039-4299	Sequence 4299, Ap
18	1711.5	42.2	672	27	US-60-360-039-9059	Sequence 9059, Ap
19	1637.5	41.9	676	27	US-60-360-039-10463	Sequence 10463, A
20	1682.5	41.2	646	27	US-60-360-039-16643	Sequence 16643, A
21	1670.5	41.2	679	27	US-60-360-039-16643	Sequence 16643, A
22	1666.5	41.1	644	22	PCT-US02-03987-5730	Sequence 5730, Ap
23	1666.5	41.1	644	22	US-09-815-242-5730	Sequence 5730, Ap
24	1666.5	41.1	644	24	US-10-072-851-5730	Sequence 5730, Ap
25	1666.5	41.1	644	27	US-60-242-578-1009	Sequence 1009, Ap
26	1666.5	41.1	644	27	US-60-253-625-2353	Sequence 2353, Ap
27	1666.5	41.1	644	27	US-60-257-931-3312	Sequence 3312, Ap
28	1666.5	41.1	644	27	US-60-269-308-4336	Sequence 4336, Ap
29	1655.5	40.8	517	18	US-09-417-507-37934	Sequence 37934, A
30	1595.5	39.3	668	27	US-60-360-039-8819	Sequence 8819, Ap
31	1586	39.1	469	27	US-60-360-039-15002	Sequence 15002, A
32	1555	38.3	534	24	US-10-015-127-10081	Sequence 10081, A
33	1548.5	38.2	469	21	US-09-791-537-20646	Sequence 20646, A
34	1545.5	38.1	469	21	US-09-791-537-33097	Sequence 33097, A
35	1529.5	37.7	471	27	US-60-360-039-19706	Sequence 19706, A
36	1520.5	37.5	526	17	US-09-328-352-8024	Sequence 8024, Ap
37	1508	37.2	672	27	US-60-360-039-7323	Sequence 7323, Ap
38	1507.5	37.2	474	1	PCT-US02-03987-5127	Sequence 5127, Ap
39	1507.5	37.2	474	22	US-09-815-242-5127	Sequence 5127, Ap
40	1507.5	37.2	474	24	US-10-072-851-5127	Sequence 5127, Ap
41	1507.5	37.2	474	27	US-60-253-625-2683	Sequence 2683, Ap
42	1507.5	37.2	474	27	US-60-257-931-3511	Sequence 3511, Ap
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44	1507.5	37.2	480	16	US-09-252-991A-28668	Sequence 28668, A
45	1494	36.8	670	27	US-60-360-039-4565	Sequence 4565, Ap
46	1483.5	36.6	466	21	US-09-791-537-15038	Sequence 15038, A
47	1483.5	36.6	481	18	US-09-489-039A-12322	Sequence 12322, A
48	1481.5	36.5	466	21	US-09-791-537-26234	Sequence 26234, A
49	1479.5	36.5	466	1	PCT-US02-03987-10021	Sequence 10021, A
50	1479.5	36.5	466	21	US-09-791-537-28986	Sequence 28986, A
51	1479.5	36.5	466	22	US-09-815-242-10021	Sequence 10021, A
52	1479.5	36.5	466	24	US-10-072-851-11164	Sequence 11164, A
53	1471	36.3	469	1	PCT-US02-03987-11164	Sequence 11164, A
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55	1471	36.3	469	22	US-09-815-242-11164	Sequence 11164, A
56	1471	36.3	469	24	US-10-072-851-11164	Sequence 11164, A
57	1467.5	36.2	470	16	US-09-252-691-9422	Sequence 9422, Ap
58	1467.5	36.2	466	16	US-09-252-691C-9422	Sequence 9422, Ap
59	1450.5	35.8	466	1	PCT-US02-03987-14017	Sequence 14017, A
60	1450.5	35.8	466	22	US-09-815-242-14017	Sequence 14017, A
61	1450.5	35.8	466	24	US-10-072-851-14017	Sequence 14017, A
62	1444.5	35.6	495	27	US-60-128-476-3203	Sequence 3203, Ap
63	1439.5	35.5	487	19	US-09-543-681A-7031	Sequence 7031, Ap
64	1432	35.3	465	21	US-09-791-537-84859	Sequence 84859, A
65	1413	34.8	485	21	US-09-791-537-82611	Sequence 82611, A
66	1399.5	34.5	475	21	US-09-791-537-104234	Sequence 104234, A
67	1399.5	34.5	475	21	US-09-791-537-82633	Sequence 82633, A
68	1385.5	34.2	476	21	US-09-791-537-109236	Sequence 109236, A
69	1385	34.2	473	21	US-09-791-537-70386	Sequence 70386, A
70	1383.5	34.1	471	21	US-09-791-537-80849	Sequence 80849, A
71	1354.5	33.4	466	21	US-09-791-537-74515	Sequence 74515, A
72	1354	33.4	466	21	US-09-791-537-74486	Sequence 74486, A
73	1354	33.4	469	21	US-09-791-537-78978	Sequence 78978, A
74	1347.5	33.2	481	21	US-09-738-626-4952	Sequence 4952, Ap
75	1330	32.8	471	21	US-09-791-537-50448	Sequence 50448, A
76	1330	32.8	553	20	US-09-606-740A-266	Sequence 266, App
77	1321.5	32.6	384	21	US-09-739-449-11127	Sequence 11127, A
78	1321.5	32.6	384	22	US-09-803-110-11127	Sequence 11127, A
79	1316	32.5	534	20	US-09-606-740A-268	Sequence 268, App

80 1311.5 32.3 470 21 US-09-791-537-58954 Sequence 55954, A
81 1304.5 32.2 464 21 US-09-791-537-108096 Sequence 108096, A
82 1300.5 32.1 461 18 US-09-450-969-6326 Sequence 6326, Ap
83 1290.5 31.8 466 21 US-09-791-537-90886 Sequence 90886, A
84 1282 31.6 456 1 PCT-US02-03987-12156 Sequence 12156, A
85 1282 31.6 456 1 PCT-US02-03987-12928 Sequence 12928, A
86 1282 31.6 456 12 US-08-827-356-5398 Sequence 5398, Ap
87 1282 31.6 456 20 US-09-611-523-6093 Sequence 6093, Ap
88 1282 31.6 456 22 US-09-815-242-12156 Sequence 12156, A
89 1282 31.6 456 22 US-09-815-242-12928 Sequence 12928, A
90 1282 31.6 456 24 US-10-072-851-12156 Sequence 12156, A
91 1282 31.6 456 24 US-10-072-851-12928 Sequence 12928, A
92 1282 31.6 456 24 US-09-540-2098-10069 Sequence 10069, A
93 1209.5 29.8 472 21 US-09-791-537-4868 Sequence 4868, Ap
94 1181.5 29.1 468 21 US-09-791-537-15039 Sequence 15039, A
95 1178.5 29.1 467 27 US-60-360-039-19849 Sequence 19849, A
96 1172.5 28.9 463 27 US-60-360-039-18971 Sequence 18971, A
97 1141.5 28.2 460 21 US-09-791-537-81237 Sequence 81237, A
98 1132.5 27.9 460 27 US-60-360-039-18414 Sequence 18414, A
99 1114 27.5 459 21 US-09-791-537-131423 Sequence 131423, A
100 1076 26.5 287 18 US-09-417-507-37932 Sequence 37932, A

ALIGNMENTS

RESULT 1
US-10-010-227-3
; Sequence 3, Application US/10010227
; GENERAL INFORMATION:
; APPLICANT: Hamer, Lisbeth
; APPLICANT: Adachi, Kiichi
; APPLICANT: DeZwaan, Todd M
; APPLICANT: Lo, Sze Chung C
; APPLICANT: Montenegro-Chamorro, Maria V
; APPLICANT: Frank, Sheryl A
; APPLICANT: Darveaux, Blaise A
; APPLICANT: Mahanty, Sanjoy K
; APPLICANT: Heiniger, Ryan W
; APPLICANT: Skalchunes, Amy R
; APPLICANT: Pan, Huiqin
; APPLICANT: Tarpey, Rex
; APPLICANT: Shuster, Jeffrey R
; APPLICANT: Tanzer, Matthew M
; TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF INHIBITORS OF 3-ISOPROPYLMALATE
; TITLE OF INVENTION: DEHYDRATASE AS ANTIBIOTICS
; FILE REFERENCE: 2131US
; CURRENT APPLICATION NUMBER: US/10/010,227
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 778
; TYPE: PRT
; ORGANISM: Magnaporthe grisea
US-10-010-227-3

Query Match 100.0%; Score 4055; DB 24; Length 778;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 778; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MFGASTPOTLYDKVLOAHVDEKLDGTLLYIDRHLVHEVTSPOAFEGLNAGRKVRP 60
Db 1 MFGASTPOTLYDKVLOAHVDEKLDGTLLYIDRHLVHEVTSPOAFEGLNAGRKVRP 60
Qy 61 DCTLATDHNVPPTSRSKALKDIASFIEDDSRTQCVTLEENKVEFGVTYFGLSDKRGQIV 120
Db 61 DCTLATDHNVPPTSRSKALKDIASFIEDDSRTQCVTLEENKVEFGVTYFGLSDKRGQIV 120
Qy 121 HVIGPEQGTFLGTTVCGDSTSTHGAFALAFGIGTSEVHVLAQTCLITKRSKNMRI 180
Db 121 HVIGPEQGTFLGTTVCGDSTSTHGAFALAFGIGTSEVHVLAQTCLITKRSKNMRI 180

Qy 181 QVDGELAPGVSSKDVVLAHIGIITAGCTGAVIEFCGVSIRLSMEARMSICNMSIEGGA 240
Db 181 QVDGELAPGVSSKDVVLAHIGIITAGCTGAVIEFCGVSIRLSMEARMSICNMSIEGGA 240
Qy 241 RAGWVAPDEITFEYLKGRPLAPKYDSPEWHKATQWKNLQSDPGAKYDIDVFTDAKDIVP 300
Db 241 RAGWVAPDEITFEYLKGRPLAPKYDSPEWHKATQWKNLQSDPGAKYDIDVFTDAKDIVP 300
Qy 301 TLTWGTSPEDVVPITGVVPDPETPATEAKADGRRLQYMGKAGTTPMEDIPVDKVFIS 360
Db 301 TLTWGTSPEDVVPITGVVPDPETPATEAKADGRRLQYMGKAGTTPMEDIPVDKVFIS 360
Qy 361 CTNSRIEDLRAAAAIVVGRKKAPNVKSAWVPGSLVKTQAEELGDKIFEAGFEWREA 420
Db 361 CTNSRIEDLRAAAAIVVGRKKAPNVKSAWVPGSLVKTQAEELGDKIFEAGFEWREA 420
Qy 421 GCSMCLGNPNPILAPOERCASSTNRNFRGCGAGRTTHLMSPVMAAAAGIVGKLADVRKL 480
Db 421 GCSMCLGNPNPILAPOERCASSTNRNFRGCGAGRTTHLMSPVMAAAAGIVGKLADVRKL 480
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Db 661 IKDQAQIEAIAAEARAGKEIEVDLPNQLIKNATGETICTFEVEEFKHCVLNGLDDIGLT 720
Qy 721 MOMEKDKAEFEAKMTRETPWLDGTGYLKRGGGKLAAKAVPVTNNRGEKKEPLEW 778
Db 721 MOMEKDKAEFEAKMTRETPWLDGTGYLKRGGGKLAAKAVPVTNNRGEKKEPLEW 778

RESULT 2
US-60-360-039-3233
; Sequence 3233, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 3233
; LENGTH: 840
; TYPE: PRT
; ORGANISM: Neurospora crassa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(840)
; OTHER INFORMATION: unsure at all Xaa locations
US-60-360-039-3233

Query Match 83.8%; Score 3397; DB 27; Length 840;
Best Local Similarity 77.8%; Pred. No. 0;
Matches 655; Conservative 53; Mismatches 60; Indels 74; Gaps 5;
Qy 9 QTLYDKVLOAHVDEKLDGTLLYIDRHLVHEVTS----- 44
Db 1 RTLYDKVFOAHIVDEKLDGTLLYIDRHLVHEVTSVRSLNPHAGELFRSPVPSTDPKS 60

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QY      45 -OAEGLRNAGKVRPDCCTLATTDH----- 69
      61 IQAEGLRNAGKVRPDCCTLATTDHVSMSLPLFEYFMAAHAFAHPXYLAPDSQSLG 120
QY      70 -----NVPTSRKALKDIAFIKEDSRQCCTLLENVKEFGVTYFGLSDPKRGI 119
      121 TASXPRTRCRNAVPTSRKALKDIAFIKEDSRQCCTLLENVKEFGVTYFGLSDPKRGI 180
QY      120 VHVYEGROGFTLPCTVAVCGSHSTHGAFGALAFGICTSEVENHLATQCLITKRSKMR 179
      181 VHVYEGROGFTLPCTVAVCGSHSTHGAFGALAFGICTSEVENHLATQCLITKRSKMR 240
QY      180 IOVDGELAPGVSSKDVVLAHAIIGITAGTGAVIEFCGSVIRLSMEARMSICNMSIEGG 239
      241 VOVDGELAPGVSSKDVVLAHAIIGITAGTGAVIEFCGSVIRLSMEARMSICNMSIEAG 300
QY      240 ARAGMVADEITFEYLKGRPLAPKXDSPEMHKATQYWKLOSDPAKXIDIVFIDAKIV 299
      301 ARAGMVADEITFEYLKGRPLAPRGSEENKAVVYWKSLASDPKXIDIVFIDAKI 360
QY      300 PTLWGTSPEDVVPITGVVPDPETPAEAKKADGRMLQYMGKAGTPEMEDI PVDKVF 359
      361 PTLWGTSPEDVVPITGVVPDPETPAEAKKADGRMLQYMGKAGTPEMEDI PVDKVF 420
QY      360 SCTNSRIEDLRRAAAVAVGKKAAPNVKSGAMVPGSLVKTQAEEDGLDKIPEEAGFEWRE 419
      421 SCTNSRIEDLRRAAAVAVGKKAAPNVKSGAMVPGSLVKTQAEEDGLDKIPEEAGFEWRE 480
QY      420 AGCSMCLGMPDILAPORCASTSNRNEFGROGAGRTHLMSPVMAAAAGIVKLAADVRK 479
      481 AGCSMCLGMPDILAPORCASTSNRNEFGROGAGRTHLMSPVMAAAAGIVKLAADVRK 540
QY      480 LTDVYASPHIAV---OKSTVYKPHVDERINODAEHKOIADIPEDNNGPHTNTSASVCT 536
      541 LTDVYASPHIAV---OKSTVYKPHVDERINODAEHKOIADIPEDNNGPHTNTSASVCT 598
QY      537 SAGLPKFTILKGIAPLEKAVNDTDALIPKQFLTKIKRTGLGNALFEYEMRFNEDGTEKSD 596
      599 SAGLPKFTILKGIAPLEKAVNDTDALIPKQFLTKIKRTGLGNALFEYEMRFNEDGTEKSD 658
QY      597 FVLNKEPRKASILVCTGANFGCGSSREHAPWALNDFGIRSVIASEFADIPFNNSFKXGM 656
      659 FVLNKEPRKASILVCTGANFGCGSSREHAPWALNDFGIRSVIASEFADIPFNNSFKXGM 718
QY      657 LPIPIKDOAQIEAIAEABRAGEIEVDLPNOLIKNATGETICTFEVEBERKXCLVNGLDD 716
      719 LPIPIKDOAQIEAIAEABRAGEIEVDLPNOLIKNATGETICTFEVEBERKXCLVNGLDD 778
QY      717 IGLTWQMEDKIAFEAKMTRETPMLDGTGLYLRKKGQGLAKAAVAVPTTNRGEEKKEPL 776
      779 IGLTWQMEDKIAFEAKMTRETPMLDGTGLYLRKKGQGLAKAAVAVPTTNRGEEKKEPL 838
QY      777 EW 778
      839 EW 840

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RESULT 3
 US-60-039-21952
 ; Sequence 21952, Application US/60360039
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Chen, Xianfeng
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; FILE REFERENCE: 38-10(52052)A
 ; CURRENT APPLICATION NUMBER: US/60/360,039
 ; CURRENT FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 21952
 ; LENGTH: 779
 ; TYPE: PR
 ; ORGANISM: Saccharomyces cerevisiae
 ; US-60-039-21952

Query Match 60.6%; Score 2456.5; DB 27; Length 779;
 Best Local Similarity 63.1%; Pred. No. 5.3e-226;
 Matches 486; Conservative 93; Mismatches 152; Indels 39; Gaps 10;

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QY      8 POTLYDKVLAHVVDKEDGTLLVYIDRLVHEVTSPOAFEGELRNAGKVRPDCCTLAT 67
      9 PRTLYDKVLAHVVDKEDGTLLVYIDRLVHEVTSPOAFEGELRNAGKVRPDCCTLAT 68
QY      68 DHNVPTSRKALKDIAFIKEDSRQCCTLLENVKEFGVTYFGLSDPKRGI VHVYEGRO 127
      69 DHNVPTSRKALKDIAFIKEDSRQCCTLLENVKEFGVTYFGLSDPKRGI VHVYEGRO 128
QY      128 GFTLPCTVAVCGSHSTHGAFGALAFGICTSEVENHLATQCLITKRSKMRIOVDGELA 187
      129 GFTLPCTVAVCGSHSTHGAFGALAFGICTSEVENHLATQCLITKRSKMRIOVDGELA 188
QY      188 PGVSKDVVLAHAIIGITAGTGAVIEFCGSVIRLSMEARMSICNMSIEGARAGVAVP 247
      189 PGVSKDVVLAHAIIGITAGTGAVIEFCGSVIRLSMEARMSICNMSIEGARAGVAVP 248
QY      248 DEITFEYLKGRPLAPKXDSPEMHKATQYWKLOSDPAKXIDIVFIDAKIVPITLWGT 307
      249 DEITFEYLKGRPLAPKXDSPEMHKATQYWKLOSDPAKXIDIVFIDAKIVPITLWGT 306
QY      308 PEDVVPITGVVPDPETPAEAKKADGRMLQYMGKAGTPEMEDI PVDKVFISGCTNSRIE 367
      307 PEDVVPITGVVPDPETPAEAKKADGRMLQYMGKAGTPEMEDI PVDKVFISGCTNSRIE 366
QY      367 DLRRAAAVAVGKKAAPNVKSGAMVPGSLVKTQAEEDGLDKIPEEAGFEWREAGCSMCLG 427
      368 DLRRAAAVAVGKKAAPNVKSGAMVPGSLVKTQAEEDGLDKIPEEAGFEWREAGCSMCLG 426
QY      428 MNPDIAPORCASTSNRNEFGROGAGRTHLMSPVMAAAAGIVKLAADVRKLTLYK--- 484
      427 MNPDIAPORCASTSNRNEFGROGAGRTHLMSPVMAAAAGIVKLAADVRKLTLYK--- 485
QY      485 -ASPHI-----AAYOKSTVTKPHVDERINODAEHKOIADIPEDNNGPHTNTS 531
      486 -ASPHI-----AAYOKSTVTKPHVDERINODAEHKOIADIPEDNNGPHTNTS 531
QY      532 ASVTSAGLPKFTILKGIAPLEKAVNDTDALIPKQFLTKIKRTGLGNALFEYEMRFNEDG 591
      542 ASVTSAGLPKFTILKGIAPLEKAVNDTDALIPKQFLTKIKRTGLGNALFEYEMRFNEDG 596
QY      592 ---TEKSPFVLNKEPRKASILVCTGANFGCGSSREHAPWALNDFGIRSVIASEFADIF 648
      597 ---TEKSPFVLNKEPRKASILVCTGANFGCGSSREHAPWALNDFGIRSVIASEFADIF 656
QY      649 NNSFKXGMIPRIKDOAQIEAIAEABRAGEIEVDLPNOLIKNATGETICT- FEVEBERK 707
      657 NNSFKXGMIPRIKDOAQIEAIAEABRAGEIEVDLPNOLIKNATGETICT- FEVEBERK 716
QY      708 HCLVNGLDIGITLMQMEDKIAFEAKMTRETPMLDGTGLY-----KRX 750
      717 HCLVNGLDIGITLMQMEDKIAFEAKMTRETPMLDGTGLY-----KRX 766

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RESULT 4
 US-10-179-131-6614
 ; Sequence 8614, Application US/10179131
 ; GENERAL INFORMATION:
 ; APPLICANT: HARE, ROBERTA S.
 ; APPLICANT: SHAW, KAREN J.
 ; APPLICANT: SHIMER JR., GEORGE H.
 ; APPLICANT: KESSLER, MARCO
 ; APPLICANT: NOLLING, JORR
 ; APPLICANT: ZENG, QIANDONG

; APPLICANT: GREENE, JONATHAN R.
; TITLE OF INVENTION: CANDIDA ALBICANS NUCLEIC ACIDS AND POLYPEPTIDES,
; FILE REFERENCE: 2976-4031
; CURRENT APPLICATION NUMBER: US/10/179,131
; CURRENT FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 10194
; SEQ ID NO 8614
; LENGTH: 794
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-179-131-8614

Query Match 60.5%; Score 2451.5; DB 25; Length 794;
Best Local Similarity 61.6%; Pred. No. 1.8e-235;
Matches 491; Conservative 90; Mismatches 167; Indels 49; Gaps 14;
QY 8 PQLYDKVLQAHVVDEKLDGTVLLYIDRHLVHEVTSPOAFGLRNAGRKVRPPDCTLTAT 67
DB 21 PKLYDKVFDHVVHKKDSSGYLLYIDRHLVHEVTSPOAFGLRNAGRSVARTDCTLTATV 80
QY 68 DHNVPTTSRKALDIASFIKEDDSRTQCVTLEENVKEFGVTYFGLSKRQGIHVHVGPEQ 127
DB 81 DHNIPTISRAFPKNVDSFIEQDSRLQVKTLEQNVKDFDVTYFGMTDRQGIHVHVGPEQ 140
QY 128 GFTLPCTTVCGDSHTSTHGAFAFALAGIGTSEVHVLAQTCLITKRSKNMRIQVDSGELA 187
DB 141 GFTLPCTTVCGDSHTSTHGAFAFALAGIGTSEVHVLAQTCLITKRSKNMRIQVDSGELA 200
QY 188 PGVSSKDVVLHAIGITAGTGAVIEFCGVSIRLSMEARMSICNNISIEGARAGVAP 247
DB 201 EGITSKDLVHLVIGVITAGTGCVIEFAGKALENLSMEARMSICNNISIEGARAGVAP 260
QY 248 DEITPEYLKGRPLAPKYDSPWEHKAQYKWNLOSQDPGAKYDIDVIDAKDIPVTLTWGTS 307
DB 261 DDTTFNYIKGRPLAPK--GQEWKAMKYKTLHTDEGAKFDYDIKIAASDIPVTLTWGNS 318
QY 308 PEDVPIITGVPPPEFATEAKKADGRMLQYMGKAGTGMEDIPVVKVFGSCTNSRIE 367
DB 319 PQDALPITASVPPATVTPDIKKSGBERALKYQGLTPTNTPFKEIKDKAFIGSCTNSRIE 378
QY 368 DLRAAAVVKGRKAPNVKSMVVPVSGLVKTOAEERGLDKIPFEEAGFEWREAGSCMLG 427
DB 379 DLRAAKVAKGKKADNVKLVVVPVSGLVKTOAEERGLDKIPFEEAGFEWREAGSCMLG 438
QY 428 MNPDLAPERCASSTNRNPEFGQAGGRTHLSPVMAAAAGIVGKLADYRKLTDYKASPHI 487
DB 439 MNPDLAPERCASSTNRNPEFGQAGGRTHLSPVMAAAAGIVGKLADYRKLTDYKASPHI 493
QY 488 HTAAVQKSTVTKPH--VDERINQDA---HEKDIITADIPE-----DNNGPHNTSASV 534
DB 494 --ATQDEPQIQIAHEIEDKELQEAHYEKEBYIEDTPQAEERLEDIPKDEPEFKRTE 551
QY 535 --GTSAGL-----KFTILKGIAPLEKANVDTDAIIPKQFLKTIKRTGLGNALFYEMRF-- 587
DB 552 IDNSAAGTSDINSFKVLGTITAPLYKANVDTDAIIPKQFLKTIKRTGLKDGFLYELRFV 611
QY 588 --NEDGTE--KSDFVLNKEPYRKASILVCTGANFCGSSREHAPWALNDFGIRSVIAPSPAD 645
DB 612 KGENGKDVETDFVLTPEPYRKAEILLVTDGNFCGSSREHAPWALNDFGIRSVIAPSPAD 671
QY 646 IFNNNSFKNGMLPIPIKQQAQIAEIAAEARAGKEIEVDLPNQLIKNATGET----ICTFE 701
DB 672 IFNNNSFKNPLPIPIQBEIISKLVVVTSGHRLTIDLPNQOIRD--GETDEVLEHFD 729
QY 702 VEEFRKHCLVNGLDDIGLTQWQEDKIAEPEAKMTRTPMDLDTGTYLKRKQGGKLAQAV 761
DB 730 VEEFRKHCLVNGLDDIGLTQWQEDKIAEPEAKMTRTPMDLDTGTYLKRKQGGKLAQAV 777
QY 762 PVPPTNRGEKEKPELEW 778
DB 778 PIKGTKKSIYGNRAQEW 794

RESULT 5
US-09-791-537-121852
; Sequence 121852, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEM
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 121852
; LENGTH: 644
; TYPE: PRT
; ORGANISM: Mucor racemosus
US-09-791-537-121852

Query Match 51.2%; Score 2076; DB 21; Length 644;
Best Local Similarity 68.8%; Pred. No. 6e-198;
Matches 407; Conservative 60; Mismatches 111; Indels 14; Gaps 6;
QY 10 TLYDKVLQAHVVDEKLDGTVLLYIDRHLVHEVTSPOAFGLRNAGRKVRPPDCTLTATDH 69
DB 51 TLYDKVMDHDVDOQEDGTCCLIIYIDRHLVHEVTSPOAFGLRNANRPVRRPDCCTLATVDH 110
QY 70 NVPPTSRKALDIASFIKEDDSRTQCVTLEENVKEFGVTYFGLSKRQGIHVHVGPEQ 129
DB 111 NIPTTRKIFKNITTFIKEDDSRTQCVTLEENVKEFGVTYFGLSKRQGIHVHVGPEQ 170
QY 130 TLPCTTVCGDSHTSTHGAFAFALAGIGTSEVHVLAQTCLITKRSKNMRIQVDSGELAPG 189
DB 171 TLPCTTVCGDSHTSTHGAFAFALAGIGTSEVHVLAQTCLITKRSKNMRIQVDSGELAPG 230
QY 190 VSSKDVVLHAIGITAGTGAVIEFCGVSIRLSMEARMSICNNISIEGARAGVAPDE 249
DB 231 VTSKDVVLHAIGITAGTGAVIEFCGVSIRLSMEARMSICNNISIEGARAGVAPDE 290
QY 250 ITFVYKGRPLAPKYDSPWEHKAQYKWNLOSQDPGAKYDIDVIDAKDIPVTLTWGTSPE 309
DB 291 VTFYLRKDKPLAPK--GADWRAVYKWSLSDADAKYDIDVIDAKDIPVTLTWGTSPE 348
QY 310 DWVPIITGVPPPEFATEAKKADGRMLQYMGKAGTGMEDIPVVKVFGSCTNSRIEDL 369
DB 349 DWVPIITGVPPPEFATEAKKADGRMLQYMGKAGTGMEDIPVVKVFGSCTNSRIEDL 408
QY 370 RAAAVVKGRKAPNVKSMVVPVSGLVKTOAEERGLDKIPFEEAGFEWREAGSCMLGN 429
DB 409 RAAAVVKGRKAPNVKSMVVPVSGLVKTOAEERGLDKIPFEEAGFEWREAGSCMLGN 467
QY 430 PDILAPERCASSTNRNPEFGQAGGRTHLSPVMAAAAGIVGKLADYRKLTDYKASPHI 489
DB 468 PDILAPERCASSTNRNPEFGQAGGRTHLSPVMAAAAGIVGKLADYRKLTDYKASPHI 520
QY 490 AAYOKSTVTKPHVDERINQDAHEKDIITADIPEDDNNGPHNTSASVGTSGAGLPKFTILKGI 549
DB 521 SEIPGTTPKQSPQEVVAEFESEEDV--DSSSVDSAP--VATPPTSGDSAGMFKFTILKGI 577
QY 550 AAPLEKANVDTDAIIPKQFLKTIKRTGLGNALFYEMRFN--EDGTEKSPFVLN 600
DB 578 AAPLDISNVDTDMITIPKQFLKTIKRTGLGSLFALYALRDPATGAENPQFVLN 629

RESULT 6
US-60-360-039-7864
; Sequence 7864, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.


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Db 474 IAE-----VKXERTFRPMEA-----FNTVTA 495
Qy 549 IAAPLEKANVDTAIIPKQFLTKIKRTGLGNALFYEMRF-----NEDGTEKSDFVL 599
Db 496 IYAPLDRANVDTAIIPKQFLSKISGSGFNPFLDEWRYLDQOGPKSGNEGRPLNKDFVL 555
Qy 600 NKEPYRKASILVCTGANFCGSSREHAPWALNDFGIRSVIAPSFADIFFNNSFKNGMLPI 659
Db 556 NLPYAGARILLARD-NFGCGSSREHAPWALQDFGRVLIAPSFADIFFNNSFKNGMLPI 614
Qy 660 PIKDOAQIEIAAE--ARAGKEIEVDLPNOLIKNATGETICTEVEEFRRKHCLVNGLDDI 717
Db 615 -VOEASVDSLSFAEVAAPQGYQITVDLPAQRIITTPSGRSI-AFEVDPRKHCLHGLDDI 672
Qy 718 GLTQMOMEDKIAEFAKWTRETPW 740
Db 673 GLTLQHVADIQAYESKHGQAPW 695

RESULT 8
US-60-360-039-15849
; Sequence 15849, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 15849
; LENGTH: 710
; TYPE: PRT
; ORGANISM: Xanthomonas campestris
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(710)
; OTHER INFORMATION: unsure at all Xaa locations
US-60-360-039-15849

Query Match 50.0%; Score 2027.5; DB 27; Length 710;
Best Local Similarity 56.4%; Pred. No. 5.3e-193;
Matches 421; Conservative 87; Mismatches 191; Indels 47; Gaps 11;

Qy 7 TPOTLYDKVLQAHVDEKLDGTVLLYIDRHLVHEVTSPOAFEGELRNAGRKVRPDCTLAT 66
Db 1 TAKTLYDKLWEMHEVTRDDGSSLIYIDRHLVHEVTSPOAFEGELRLAGRKVPWRIDANIAT 60
Qy 67 TDHNVPTTSRKALDKTASFKEDDSRTQCVTLLENVKEFGVTVYFGLSDKRGQIVHVIGPE 126
Db 61 PDHNVPTTRAEROGGLES-ISDEVSRLOVQTLDENCDDFGILEFKMDTQGIHVHVIGPE 119
Qy 127 QGFTLPGTTVCCGSDSTHGAFCALAFGIGTSEVEHVLATQCLITKRSKNMRLQVDDGEL 186
Db 120 QGATLPGMTVCCGSDSTHGAFCALAHGIGTSEVEHVLATQCLIAKKMKNQVRVBGTL 179
Qy 187 APGVSSKDVVLHAIGIIGTAGGTGAVIEFCGSVIRSLSMERMSICNMSIEGGARAGMVA 246
Db 180 PFGVTAKDVLAVIGKIGTAGGNHGALEFAGSIRAIRALSMEGRMTCNMSIEAGARVMVA 239
Qy 247 PDEITEYLKGRPLAKYDSEPHKATQYWKNLQSDPGAKYDIDVFDKDIIVPTLTWGT 306
Db 240 VDEKTIAYKGRFBAPK--GADWDAAVALWRLTLVSDADASFDTVVEURASDIKQVSWG 297
Qy 307 SPEDVVPIGVDPDPETFAEAKKADGRRLMQYMLGAKGFMEDI PVDKVFIGSCTNSRI 366
Db 298 SPWMVVAIDQVDPAAEQDPTKRDSTQRALKYMLGRANQPI TEIHLDRVFIGSCTNSRI 357
Qy 367 EDLRAAAA VVKGRKKAPNVKSAMVVPFSGSLVKTQAEEGEGLDKIFEEAGFEWREAGCSMCL 426
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Db 358 EDLRAAAA VAKGRKVASTIKQALVVPFSGSLVKAQAEAGLDFIFLDAGFEWREPGCSMCL 417
Qy 427 GMPDIIALPORCACSTSNRNFEGQAGGRTHLSPVMAAAGIVGKLADVRKLTIDYKAS 486
Db 418 AMNPDKLSGSEHCACSTSNRNFEGQAGGRTHLVSPAAAAAASVGHFVDFVRELQGIETR 477
Qy 487 PHIAAYQKSTVTKPHVDERINODAEKDI IADIPEDNNGPHTNTSASVGTSGAGLPKPTIL 546
Db 478 E--XGIATSRLLPHPH-----HSLLPPIGP-----MTPFTQH 507
Qy 547 KGIAAPLEKANVDTAIIPKQFLTKIKRTGLGNALFYEMRF-----NEDGTEKS-----DF 597
Db 508 TGLVAPLDRANVDTDQIIPKQFLSKIKRTGFGPNLDFDEWRYLDIGEPGKDNSTRPLNQBF 567
Qy 598 VLNKEPYRKASILVCTGANFCGSSREHAPWALNDFGIRSVIAPSFADIFFNNSFKNGML 657
Db 568 VLNFRYQGASVILLAR-ENFCGSSREHAPWALDEYGRAVIAPSFADIFFNNSFKNGLL 626
Qy 658 PIPKDOAQIEIAAE--ARAGKEIEVDLPNOLIKNATGETICTEVEEFRRKHCLVNGLD 715
Db 627 PI-VLAEAMDALFEQCLNGEGYQLTVDLAAQORVRRPDGVVEY-AFEIDAFRKHCLINGLD 684
Qy 716 DIGLTQMOMEDKIAEFAKWTRETPWL 741
Db 685 DIGTLQDADAIGRFEQGHRAQQPWL 710

RESULT 9
US-60-360-039-15479
; Sequence 15479, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 15479
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Xanthomonas campestris
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(711)
; OTHER INFORMATION: unsure at all Xaa locations
US-60-360-039-15479

Query Match 49.8%; Score 2018.5; DB 27; Length 711;
Best Local Similarity 56.1%; Pred. No. 4.3e-192;
Matches 419; Conservative 87; Mismatches 192; Indels 49; Gaps 10;

Qy 9 QTLVYDKVLQAHVDEKLDGTVLLYIDRHLVHEVTSPOAFEGELRNAGRKVRPDCTLATID 68
Db 2 KTLVYDKLWEMHEVTRDDGSSLIYIDRHLVHEVTSPOAFEGELRLAGRKVPWRIDANIATPD 61
Qy 69 HNVPTTSRKALKDITASFKEDDSRTQCVTLLENVKEFGVTVYFGLSDKRGQIVHVIGPEQ 128
Db 62 HNVPTTRAEROGGLES-ISDEVSRLOVQTLDENCDDFGILEFKMDTQGIHVHVIGPEQ 120
Qy 129 FTLPGTTVCCGSDSTHGAFCALAFGIGTSEVEHVLATQCLITKRSKNMRLQVDDGELAP 198
Db 121 ATLPGMTVCCGSDSTHGAFCALAHGIGTSEVEHVLATQCLIAKKMKNQVRVBGTLPP 180
Qy 189 GVSSKDVVLHAIGIIGTAGGTGAVIEFCGSVIRSLSMERMSICNMSIEGGARAGMVA 248
Db 181 GVTAKDIVLAVIGKIGTAGGNHGALEFAGSIRAIRALSMEGRMTCNMSIEAGARVMVA 240
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Qy 249 EITFEYLKGRPLAKYDPSPEHKAQYWKNUQSDPGAKYDIDVFIIDAKDLYPTLTWGTSP 308
Db 241 EKTIAVYKGRFPFAK--GADWDAVALMRTLVSADASFDTVVEILRAEDIKPQVSWGTSIP 298
Qy 309 EDVVPITGVNDPEPTFAEAKKADGRMLQYMGKAGTPMEDIPVDKVFISGCTNSRIED 368
Db 299 EMVAIIQOVDPDPAEODPTGRDSTIGRLKYMGLRANPFIIEHIDRFISGCTNSRIED 358
Qy 369 LRAAAVYKGRKKA PNYSANVVPGSGLVKTOAEEGDLKI FEEAGFEMRAGSCMCLM 428
Db 359 LRAAAVAKGRKVASITKQALVVPGSGLVKAQAEAGDLKIFLDGFEFMRBPGSCMCLAM 418
Qy 429 NPDLIAQPERCASTSNRNFEGRQAGGRTHLMSPVMAAAAGIVKLDVRLTYKASPH 488
Db 419 NPDLKSGSEHCASSTSNRNFEGRQAGGRTHLVSPMAAAAAGVFVDVREIQLJETREX 478
Qy 489 IAAQKSTVTKEPHVDERINDQAEHKDIIADIPEDNNGPHTYTSASVGTSA--GLPXFITLK 547
Db 479 GIATSRLL-----HPATPSTPMSRYSMTPTQHT 507
Qy 548 GIAPLEKANVDTDAIIPKQFLKTIKRTGLGNALFEYEMF--NEDGTEKS-----DFV 598
Db 508 GLVAFPLRANVDTQIIPKQFLKSIKRTGFGPNLFDEWRYLDIGPGRDNGSTRPLNGEFV 567
Qy 599 LNKPYPYKASILVCTGANFGCGSSREHAPMALNDFGIRSVIAPSPADI FFMNSFKNGMLP 658
Db 568 LNPFYRGASVTLAR--ENFGCGSSREHAPMALDEGFRAVIAPSPADIFYNNSFKNGMLP 626
Qy 659 IPIIDQAIETIAAE--ARAGKEIEVDLPNOLIKXATGETICTFEVEBFKHCVLNGLDD 716
Db 627 I-VLAEBMDLFEQCCAGNEGQTLVDLAQRVRKPDVEY-AFETIDFRKHCVLNGLDD 684
Qy 717 IGLTMQEMDKIAEFKAKMTRTPMLDG 743
Db 685 IGLTLQADAIGRFEQGHRAQQPWLFG 711

RESULT 10
US-60-360-039-9413
; Sequence 9413, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360, 039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 9413
; LENGTH: 752
; TYPE: PRT
; ORGANISM: Xylella fastidiosa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1) -(752)
; OTHER INFORMATION: unsure at all Xaa locations
US-60-360-039-9413

Query Match 49.2%; Score 1995; DB 27; Length 752;
Best Local Similarity 54.8%; Pred. No. 1,1e-189;
Matches 418; Conservative 96; Mismatches 207; Indels 42; Gaps 13;
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Qy 129 FTLPCTTYVCGDSHTSTHGAFALAFGISTSEVEHVLATQCLITKRSNNRIQYDGLAP 188
Db 121 ATLPQMTYVCGDSHTSTHGAFALAHGISTSEHVLATQCLVTKMKNMQRVREGTISW 180
Qy 189 GVSQKDVLAHIGITGAGGAVIEFGSVYRSLSMERMSI CNMSIEGAGARGMVAPD 248
Db 181 GTAKDVLALIGIKTGGNGVAFESGSTIRALSMERNITICMALLEAGARGMVAVD 240
Qy 249 EITFEYLKGRPLAKYDPSPEHKAQYWKNUQSDPGAKYDIDVFIIDAKDLYPTLTWGTSP 308
Db 241 EKTIOYHGRFPFAK--GSDWDAVAFVRGLVSDPDHAFDRVELSABEIKPQYTWGTSP 298
Qy 309 EDVVPITGVNDPEPTFAEAKKADGRMLQYMGKAGTPMEDIPVDKVFISGCTNSRIED 368
Db 299 EMVSAVQSVDPDERETDPVKESLIRALKYMGQPNDPISIKLDRFISGCTNSRIED 358
Qy 369 LRAAAVYKGRKKA PNYSANVVPGSGLVKTOAEEGDLKI FEEAGFEMRAGSCMCLM 428
Db 359 LRAAAVYKGRKVASITKQAMVVPGSGLVKAQAEVGBDLKIFIEAGFEMRBPSCMCLAM 418
Qy 429 NPDLIAQPERCASTSNRNFEGRQAGGRTHLMSPVMAAAAGIVKLDVRLTYKASPH 488
Db 419 NPDLKSGSEHCASSTSNRNFEGRQIGGRTHLVSPMAAAAAGVFVDVREM--MRDEPY 476
Qy 489 I-----AAYQKSTVTKEPHV-----ERINDQAEHKDIIADIPEDNNGPHTYTSASVGTSA 538
Db 477 VVPVDAWKXANEGLYSNPFEDCFNTSSAXSVSKRLFSP---AAXXGSAIYDRSA 532
Qy 539 G-----LPKFTILKGIAPLEKANVDTDAIIPKQFLKTIKRTGLGNALFEYEMF-- 587
Db 533 HRIFPMKXSLMKPFTQHTGLVCPDVRVVDTDQIIPKQFLSIKRTGFGPNLFDEWRYLD 592
Qy 588 ----NEDGTEK---SDFVANKPYRKASILVCTGANFGCGSSREHAPMALNDFGIRSVIA 640
Db 593 AGQGGQDSKRPINSDFVLANPVRGASVLLARD--NFGCGSSREHAPMALDEYGRITYIA 651
Qy 641 PSPADIFPNNSEFKNGMLPIPIKDAQIEAIAEARA--GKEIEVDLPNOLIKXATGETIC 698
Db 652 PSFADIFPNNSEFKNGMLPL-VLNKVEVDALFAQCQVTEGYTLVDLAQOVITPDGTTY- 709
Qy 699 TFEVEBFKHCVLNGLDDIGLTMQEMDKIAEFKAKMTRTPML 741
Db 710 AFQIDTFKHCVLNGLDDIGLTLQYAEIRAFETHRIQPMWL 752

RESULT 11
US-60-360-039-17883
; Sequence 17883, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360, 039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 17883
; LENGTH: 755
; TYPE: PRT
; ORGANISM: SPHINGOMONAS
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1) -(755)
; OTHER INFORMATION: unsure at all Xaa locations
US-60-360-039-17883

Query Match 48.8%; Score 1978; DB 27; Length 755;
Best Local Similarity 54.3%; Pred. No. 5,5e-188;
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; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: 38-10(52052)A
 ; CURRENT APPLICATION NUMBER: US/60/360,039
 ; CURRENT FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 8616
 ; LENGTH: 681
 ; TYPE: PR1
 ; ORGANISM: Ralstonia metallidurans
 US-60-360-039-8616

Query Match 48.2%; Score 1955.5; DB 27; Length 681;
 Best Local Similarity 53.7%; Pred. No. 8.3e-186;
 Matches 400; Conservative 96; Mismatches 174; Indels 75; Gaps 10;

QY 8 PQTLYDKVLAHVDEKLDGTVLLYIDRLVHEVTSPOAFEGRLNAGKVRPDCATLT 67
 DB 1 PASLLDKLMSHVHEQSDGSLIYIDRLVHEVTSPOAFEGRLNAGKVRPDCATLT 60
 QY 68 DHNVPTTSRKALKDIAPIKEDDSRTQCVTLEENVEFGVTVFGLSDRQGIIVHIGPEQ 127
 DB 61 DHNVPTT-----AAIDAPISSAOVDALBRNCAATGIVNFGNDRQGIIVHIGPE 114
 QY 128 GFTLPQTVVCGDSTHTGAFGALAFGIGTSEVEHVLATQCLITKRSKNMRIQVGE 187
 DB 115 GATLPQTVVCGDSTHTGAFGAFGIGTSEVEHVLATQCLITKRSKNMRIQVGE 174
 QY 188 PGVSSKDVLAHIGITGAGTGAVIEFGCVISLSMEARKSNMSIEGARGGMVAP 247
 DB 175 AGVAKDIALALIGITGAGTGAVIEFGCVISLSMEARKSNMSIEGARGGMVAV 234
 QY 248 DEIFEVYKGRPLAPKYSPMHKATQYKMLQSDPGAKYDIDVITDAKDIPVTLTWGTS 307
 DB 235 DETLAYAHNRPOAPQGA--WESASAYWRTIKRSDPAVFDVVDIGVATITREHVWTGS 292
 QY 308 PEDVPIITGVVDETFATKAKADGRMLQYMGKAGTPEMIDIVDKVFIGSCNRSIE 367
 DB 293 PEMVVAIDERIPDPQGEADPVRRGEMERALTYMGLEPGIKVASIALDKVFIGSCNRSIE 352
 QY 368 DLRAAAVVKRKAQNVKASVNVVPGSLVKTQAEFEGLDKIFEEAGGEMRAGGSMCLG 427
 DB 353 DLRAAADVLRSHVASNIRQALVNVPGSLVKSQAEAGIDRFVFDAGGEMRAGGSMCLG 412
 QY 428 MNPIILAPQECASISNPNFGROGAGRTHLMSPVMAAAGIVGKLADVRLTYKASP 487
 DB 413 MNDRILAPQECASISNPNFGROGAGRTHLVSQMAAAAAGVAGHVDV----- 462
 QY 488 HIAAYOKSTVTKPVYDERINODAHKDIADIPEDNNGPHNTSASVGTSAGLPKFTILK 547
 DB 463 -----STVLQ-----EK-----SAVKAFVLD 479
 QY 548 GIAAPLEKAVNDTDAIIPKQFLKTIKRTGLGNALFYEMRFNEDG-----TEKSDPV 598
 DB 480 GLVAPIDRANVDTDAIIPKQFLKTIKRTGLGNALFYEMRFNEDG-----TEKSDPV 539
 QY 599 LNKEBYRKAISIVCTGANFGCGSSREHAPMALNDGIRSVIAPSFADIFFNNNSFGKMLP 658
 DB 540 LNQPYQGASVYL-VRENFCCSSREHAPMALEDGRLALAPSPADIFFCNNCKMKGGLP 598
 QY 659 IPIKQAOIEAIAAE--ARAGKEIEVDLPNOLIKNATGETICTFEVEERFKCLVNGLDD 716
 DB 599 IVEANV-VDRFAVVDATPGVRLHVDLATQVTTSPSGAI-SFMDPFGKGVCLNGLDD 656
 QY 717 IGLTQMEDKIAEFAKMTRETPEML 741
 DB 657 IGLALQHEEAIRRYELNRI RHPEWL 681

RESULT 14
 US-60-360-039-7437
 ; Sequence 7437, Application US/60360039
 ; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei
 ; APPLICANT: Chen, Xianfeng
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: 38-10(52052)A
 ; CURRENT APPLICATION NUMBER: US/60/360,039
 ; CURRENT FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 7437
 ; LENGTH: 740
 ; TYPE: PR1
 ; ORGANISM: Burkholderia cepacia
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (11..740)
 ; OTHER INFORMATION: unsure at all xaa locations
 US-60-360-039-7437

Query Match 46.6%; Score 1891; DB 27; Length 740;
 Best Local Similarity 52.5%; Pred. No. 2.9e-179;
 Matches 396; Conservative 102; Mismatches 195; Indels 62; Gaps 13;

QY 34 DRHLYHEVTSPOAFEGRLNAGKVR---RPDCATLTADNVPTTSRKALKDIAPIKED 89
 DB 1 ERVYLAHTVQKDLHSLVR--GRSCXAGMRISANILASDHNVPTTDR-----SHGIADP 52
 QY 90 DSRQCVTLEENVEFGVTVFGLSDRQGIIVHIGPEGFTLPQTVVCGDSTHTGAF 149
 DB 53 ISRLQVDTLDNCDAVIGITQFPMNDLRQGIIVHIGPEGATLPQTVVCGDSTHTGAF 112
 QY 150 GALAFGIGTSEVEHVLATQCLITKRSKNMRIQVGEELAPGVSSKDVLAHIGITAGT 209
 DB 113 GALAHGIGTSEVEHVLATQCLITKRSKNMRYKVEGALRGCTARDIVAITIGITAGT 172
 QY 210 GAVIEFGCVISLSMEARKSNMSIEGARGGMVAPDEITFEYLKGRPLAPKYDSEW 269
 DB 173 GVAIEFGCVISLSMEARKSNMSIEGARGGMVAPDEITFEYLKGRPLAPKYDSEW 230
 QY 270 HKATQYKMLQSDPGAKYDIDVITDAKDIVPTLTWGTSPEDVNPITGVVDETFATK 329
 DB 231 NHAVEYWKQFSDDAQDPDRVLELMAEIVPQVWTGTPPEWTAVDGVPDPDRKDPVK 290
 QY 330 KADGRMLQYMGKAGTPEMIDIVDKVFIGSCNRSIEDLRAAAVVK--GRKAPNVKS 387
 DB 291 KDAERALKYMALEPNAPITESTIKPKITFIGSCNRSIEDLRAAAVVKKGRVAPNIRL 350
 QY 388 AMVNVGSLVKTQAEFEGLDKIFEEAGGEMRAGGSMCLGNPNILAPQECASISNPNF 447
 DB 351 AMVNVGSLVKAQAREBGIDKVFDTAGFEWREPGCSMCLANMADLFEGERCASISNPNF 410
 QY 448 EGROGAGRTHLMSPVMAAAGIVGKLADVRLTYKASPHIAAYOKSTVTK----- 499
 DB 411 EGROGAGRTHLVSPPMAAAAIEGHFVDIRLGTXTMMKNN--NRTTLNRFALGSLA 467
 QY 500 -----PHYDERINODAHKDIADIPEDNNGPHNTSASVGTSA-- 539
 DB 468 GILLGLACNTVHGFGEEDMSHSGNISNHDKXAVFDCRPAQSGFFYSLRASPLGELTGA 527
 QY 540 --LPEFTLIKGIAPLEKAVNDTDAIIPKQFLKTIKRTGLGNALFYEMRF--NEDGTEK 594
 DB 528 SVMKEFIVHTGVAPLDRENVDTAIIPKQFLKTIKRTGLGNALFYEMRF--NEDGTEK 587
 QY 595 S-----DVLNKEBYRKAISIVCTGANFGCGSSREHAPMALNDGIRSVIAPSFADIFF 648
 DB 588 SQRPPLNPDVFNQPYQGASVYLAR-KNFGCGSSREHAPMALEQYGFALALAPSFADIFF 646
 QY 649 NNSFGKMLPPIPIKQAOIEAIAEARA--GKEIEVDLPNOLIKNATGETICTFEVEER 706
 DB 647 NNCFFQGVLPVLTQ-QVDHLFNETYAFNGFKLTVLEAOVVRITADGCTEYFEVAAFR 705

Db 471 -----SP-----RRLVQP----- 479
Qy 541 PKFTILKGIAPLEKXAVNTDAIIPKQPLKTIKRTGLGNALFYEMRF---NEDGTEKS-- 595
Db 480 --FKLEALVPLDRVNVDTDAIIPKQFMKSVQNGNPGFINLFDENRYDPDHBPQGDPESTR 537
Qy 596 ---DVLNKEPYRKASILVCTGANFGCGSSREHAPMALNDGIRSVIAPSPADIFENNS 651
Db 538 RLNDPFLVNLQPRFAGAEILL-TRDNFGCGSSREHAAMALMDFGIRLIALIPGFADIFYGNC 596
Qy 652 FKNQMLPPIKDOQAQIEIAAEARA-GKEIEVDLPNOLIKNATGETICTFEVEEERKHL 710
Db 597 FKNQMLPPIKDERIVQQLFDLVGRTPGLRLAIDLEAQRIOPPAGDAI-PEFVEPERKRL 655
Qy 711 VNGLDIGLTMQMEDKIAFEAKMTRETPWL 741
Db 656 LNLGDDVALTLQOTDQIRAYERNRAHEPWL 686

RESULT 17
US-60-360-039-4299
; Sequence 4299, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 4299
; LENGTH: 688
; TYPE: PRT
; ORGANISM: Burkholderia fungorum
US-60-360-039-4299

Query Match 45.8%; Score 1857; DB 27; Length 688;
Best Local Similarity 51.3%; Pred. No. 6,6e-176;
Matches 386; Conservative 92; Mismatches 189; Indels 86; Gaps 10;

Qy 6 STPQTLVDKVLQAHVVDKLTGTVLYIDRHLVHEVTSPOAFEGLRNAGKVRPDCITL 65
Db 5 TSPRLIDKLMQSHVAVETPENGPTLLIVDRHLVETSPQAFEARLSGRKWRPEYVLA 64
Qy 66 TTDHNVPT-----TSRKALKDIAFIEDSRTOCVTLEENVKEFGVTVYFGLSDKRGIV 120
Db 65 VADHNVPTIAERTSMADIADPL-----SRIQVAQLDKCKCKEFGISYGRINPQGGII 117
Qy 121 HVIGPEGFTLPPTTVVCGDSHTSTHGAFGALAFGIGTSEVENHVLATQCLITKRSKNRI 180
Db 118 HVGVEGLATLPGMTVAVGDSHTSTHGAFALAFVGTSSEVENHVLATQCLISGKKMSMLV 177
Qy 181 QVDEGLAVGSSKDVVLAIGIIGTAGTGAVIEFGSVIRISMEARMSNNMSIEGGA 240
Db 178 NVEGFLPVGATAKDVILAIIRRTGTAGTGAVMEFAGSTIRILSMEGRITLCNNMILEGGA 237
Qy 241 RAGWAPDEITFEYELKGRPLAPKYDSPENHKAQYWKMLQSDPGAKYDIDVFIADKDIVP 300
Db 238 RVGLIGVSDVTIDYKGRFPAPA--EAHMDDAVALVWRLTVSPADARFKIVLIDATQLARP 295
Qy 301 TLVMTGSEPDVVPITGVVPDEPTFAATEAKKADGRMLQYMGILKAGTPMEDIPVDKVFIS 360
Db 296 MVTGTSSEMTVTVDDAVBNPLDDDPVVRATMAGALTYMGLEPGTSLSKSLIDIKIFIGS 355
Qy 361 CTNSRIEDLRAAAAYVVKRKKAPYKSAWVVPVSGGLVTKQAEEGGLDKIFEEAGFEMRA 420
Db 356 CTNATIEDLRAAAAYVVKRHHVAPVQLALVVPVSGGLVTKQAEAGLDAIFKAGSEWREP 415
Qy 421 GCSMCLGNPDLAPQERCASTSNRNFEGRQAGAGRTHLMSFVMAAAAGIVGKLADVRKL 480

Db 416 GCSMCLGNNDRLRPGEECASTSNRNFEGRQPGGRSHLVSPAAAAAIAIGHFYDV--- 472
Qy 481 TDYKASPHIAAYQKSTVTKPHVDERINQDAHEKDIADIPEDNNGPHTNTSASVAGL 540
Db 473 -----SHGGL 477
Qy 541 --PKFTILKGIAPLEKXAVNTDAIIPKQPLKTIKRTGLGNALFYEMRF---NEDGTEKS 595
Db 478 LVQPFTEKLEALVPLDRVNVDTDAIIPKQFMKSVQNGNPGFINLFDENRYDPDHBPQGDPS 537
Qy 596 ---DVLNKEPYRKASILVCTGANFGCGSSREHAPMALNDGIRSVIAPSPADIFEN 649
Db 538 TRRLNPDEVLNLQPRFAGAEILL-TRDNFGCGSSREHAAMALMDFGIRLIALIPGFADIFYG 596
Qy 650 NSFKQMLPPIKDOQAQIEIAAEARA-GKEIEVDLPNOLIKNATGETICTFEVEEERKHL 708
Db 597 NCFKQMLPPIKDERIVQQLFDLVGRTPGLRLAIDLEAQRIOPPAGDAI-PEFVEPERKRL 655
Qy 709 CLVNGLDIGLTMQMEDKIAFEAKMTRETPWL 741
Db 656 RLNLGDDVALTLQOTDQIRAYERNRAHEPWL 688

RESULT 18
US-60-360-039-9059
; Sequence 9059, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 9059
; LENGTH: 672
; TYPE: PRT
; ORGANISM: Chloroflexus aurantiacus
US-60-360-039-9059

Query Match 42.2%; Score 1711.5; DB 27; Length 672;
Best Local Similarity 49.2%; Pred. No. 2,6e-161;
Matches 358; Conservative 97; Mismatches 210; Indels 63; Gaps 12;

Qy 8 PQTLYDKVLQAHV-DEKLDGTVLVYIDRHLVHEVTSPOAFEGLRNAGKVRPDCITL 66
Db 1 PRTLEKXMEAHVLRPEIATPRAVLVYIDLHLIHEVTSPOAFTELRQGLRVRRPDKITLAT 60
Qy 67 TDHNVPTTSRKALKDIAFIEDSRTOCVTLEENVKEFGVTVYFGLSDKRGIVHIGPE 126
Db 61 MDHSTPTTPRNHLGIIP--VVDPMALISQLEQLRKCAEFGLIPFELIGDENOGIVHIGPE 118
Qy 127 OGFTLPPTTVVCGDSHTSTHGAFGALAFGIGTSEVENHVLATQCLITKRSKNRIOVDDGL 186
Db 119 QGLTPGMTIVCGDSHTSTHGAFGALAFGIGTSEVENHVLATQCLITKRSKNRIOVDDGL 178
Qy 187 APVSSKDVVLAIGIITAGTGAVIEFGSVIRISMEARMSIENNSIEGAGAGVVA 246
Db 179 GPGVTAKDIIILAIKAVGVGGTGVVFYMEGARIALSMEERMTICNNISIEGAGAGVVA 238
Qy 247 PDEITFEYELKGRPLAPKYDSPENHKAQYWKMLQSDPGAKYDIDVFIADKIVPLTMTGT 306
Db 239 PDDITFEYIAGRPAPK--GADFEAAVAVARWTLPEDEATPDEHETLLTASLEKPKMITTGT 296
Qy 307 SPEDVVPITGVVPDEPTFAATEAKKADGRMLQYMGILKAGTPMEDIPVDKVFISCTNSRI 366
Db 297 NFGMGIPIADAVPRPEMDPARSRALDKALAYMGLBEFGKPLGHPVDVVFVIGSCTNSRL 356

Qy	249	ETTFEYLKGRPLAPKYDSPEWHKATQYWKNLQSDPGAKYDIDVFIDAKDIDVPTLTWGTSP	308
Db	235	ETTFNYIKGREFAPK--GAKWDEAVAYWKTLYSDSDAVFDKTLUKYDAADIGPMITTYGTP	292
Qy	309	EDVVPITGVVDPDETFATEAKKADGRMLQYMGCLKAGTWMEDIPVDKVFIGSCTNSRIED	368
Db	293	GMGISVKNIPSLDSI-EESNKVTFNKALDYMGFHAGDSLIGKQVNVVFLGSCNTRIED	351
Qy	369	LRAAAVVKGRKAPNVKSAWVPGSLVKQTAEELGDKIPFEAGFEWREAGSCMCLGM	428
Db	352	LROFAEPVKGKQKAANI-NALIVPGSKQVEKQIAEIGIDKVLAEAGFELREPGCACLAM	410
Qy	429	NPDTLAPQERCASTSNRNPEGRGAGRTHLMSPVMAAAAGIVGKLADVRKLTDYKASPH	488
Db	411	NEDKVPGEYCVSTSNRNPEGRQPGARTLLVSPLTAAATAVSGKIVDVREMLNXSSNIQ	470
Qy	489	IYAYQKSTVTKPHVDERINODAEHEKDIADIPEDNNGPHTNTSASVGTSAGLPKFTILKG	548
Db	471	ISPIKR-----IXDFK-----TPTMEKFITIKS	494
Qy	549	IAPLEKANVDTAIIPKQPLKTIKRTGLGNALFYEMRFNEDTEKSDFVLNKEPRKAS	608
Db	495	TVVPLPTEVDYDQIIPAREFLKATTEGFGKSLFCDMRYNQDGTPKADFVMN-NPLYSGQ	553
Qy	609	ILVCTGANFGCGSSREHAPWALNDFGIRSVIAPSFADIFFNNSFKNGMLPIPIKD---QA	665
Db	554	ILV-AGNFGCGSSREHAAWAIGDAGFRVVVSSFFADI FRGNALNNGILLPVQVSDAFLKS	612
Qy	666	QIEAIAAEARAGKIEVDLPNQLIKNATGETICTFEVEEPRKCLVNGLLDGLTQMOMED	725
Db	613	IFDAVAANAK--QELVVDLANOVISIAAGTDLKESFVINEYKKTCLINGVDYDIDVLSIKD	670
Qy	726	KIAEFE 731	
Db	671	KIEAYE 676	
RESULT 20			
US-60-360-039-16643			
; Sequence 16643; Application US/603600039			
; GENERAL INFORMATION:			
; APPLICANT: Cao, Yongwei			
; APPLICANT: Chen, Xianfeng			
; APPLICANT: Goldman, Barry S.			
; APPLICANT: Hinkle, Gregory J.			
; APPLICANT: Slater, Steven C.			
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF			
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES			
; FILE REFERENCE: 38-10(52052)A			
; CURRENT APPLICATION NUMBER: US/60/360,039			
; CURRENT FILING DATE: 2002-02-21			
; NUMBER OF SEQ ID NOS: 47374			
; SEQ ID NO 16643			
; LENGTH: 646			
; TYPE: PRI			
; ORGANISM: Bacillus thuringiensis			
US-60-360-039-16643			
Query Match 41.5%; Score 1682.5; DB 27; Length 646;			
Best Local Similarity 49.7%; Pred. No. 1.9e-158;			
Matches 359; Conservative 87; Mismatches 196; Indels 81; Gaps			
Qy	11	LYDKVLQAHVVDKLGDTGLLYITDRHLVHEVTSQPAFEGRLNAGRKVRPDCDTLATTDHN 70	
Db	5	LLDKLWERHVVATNENGLDLYITDLHLVHEVTSQPAFEGRLRLNRTVRRPDLTFAATMDHN 64	
Qy	71	VPTTSRKALDXIAFTKEDDSRTCQVTLLENVKEFGVTFGLSKRQGIWHVIGPQOGFT 130	
Db	65	IPT-----KDVWN--ITDRIAKQOLDTLRENCKQFQVPLADIGDEFGQGIWHVIGPELGLT 117	
Qy	131	LPGTTVVVCGDSHTSTHGAFALPGIGTSEVHEVLATQCLITKRSKNMRIQVDDGELAPGV 190	

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Db 118 QPKKTI VCGDSHTATGAFALAFGICTSEVENHLAQTLMQRPKAMGIELKGLPGCV 177
Qy 191 SKSDVVAHAIIGITGAGTCVATIEFGGSVIRLSLMEARMSICNNSIBGADPAGVAPEI 250
Db 178 YAKDIIHLHLSTKGVAVGTGYVMEFYGEALHAMMEERMTLCNNAIEBGAKAIGIAPDEK 237
Qy 251 TFEYIKGRPLAPYDSEPMHKAQTQWKNLQSDPAKXDIDVFIADKDIVPLTLTWTGSPED 310
Db 238 TAAVYAKGRXYAPF---DYESIKKWSELTDTDLAVYDLHLVDTDLAPVYTWGTSNBSM 293
Qy 311 VVPIGTVPDPEPFATEAKKADGRMLQYNGLKAGTEMEDIPVDKVFISGCTNSRIEDLR 370
Db 294 GVRIDEKPL-----EKHDANDERAFSTWGLSPGQSTYDIPQGHVFIQSCTNSRLSDLE 346
Qy 371 AAAAVYKGRKKAPNVKSAMVYFGSGLVYQTQAEERGLDKIFEEDAGFEWREBAGCSNCLGNAP 430
Db 347 TAAVYKGRKKVKEGVR-ALVVPQSQRVREAAAHKGLHRIFEEDAGFEWREBAGCSNCLGNAP 405
Qy 431 DILAPOERCASSTNSRNFPEGRQAGAGRTHLSPVMAAAAGIYGLKADVARKLTDYKASPHIA 490
Db 406 DQVPEGECHASTSNNRNFEGRQAGKARTHLVSPMAAAALALGHFVDIRK----- 454
Qy 491 AYQKSTVTKPHYDERINQDAHEKDIADIDEDNNGPHTNTSASVQTSAGLPKFTILKQIA 550
Db 455 -----ESYDG-----AFRIHKQTA 468
Qy 551 APLEKANVTDDAIIPQOFLKTIKRTGIGLGNALFYEMRPNREDQTEKSDPVLNKEPYKASIL 610
Db 469 APLMNDINDITDOIIPQOYLRIERTGFGKFLFDMRWDRDNNQENPFLNQERKASIL 528
Qy 611 VCTGANFGCGSSREHAPMALNDPGRSIVAPSPADIFENNSFKKGMLEPIPIKDOAQIEAI 670
Db 529 I-TGDNFGCGSSREHAPMALADYGFRIYIAGGFADIFIMCMKGMLEI-VMDKMRQOL 586
Qy 671 AAEEARAKEIEVDLPNOLIKMATGETICTFEVEEERKGLVNGLDIGLTMQMEDKIAEF 730
Db 587 -AKTDAREQITVDLENEIMTNTTHR--FHFTIEKMKKEKLLNGLDEISITWQYEQEIKEX 643
Qy 731 EAK 733
Db 644 ERK 646

RESULT 21
US-60-360-039-14041
; Sequence 14041, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 14041
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Pseudomonas fluorescens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(679)
; OTHER INFORMATION: unsure at all Xaa locations
US-60-360-039-14041

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Db      1  RTLYKHADSHVCTLDDO--GHVLLYIDROYANETTSPOAFESGLFEAGTWTWRPATTLA 58
Qy      66  TTDHNVPTTSRKALXDIAFIFIKEDDSRTQCVTLLENVKEGVTFGLSDRKQIVHVG 125
Db      59  VVDHVNPT-----APRIATMPDAGGAR-QVSYFEENCRDPGIELFDVLDRKQIEHVAP 113
Qy      126  EOGFTLPCTTVVCGSHSTHAGAFGALAFGIGTSVEVHVLATQCLITKSKNMRIQVDGE 185
Db      114  EOGFTLPGVNVVAAGSHHTTYGALGARFGIGTSEIEHLATQTVLYKRTKRTLVNNGE 173
Qy      186  LAPGSSKQVNVHAIGIITAGTGAVIEFCGVSISLSWEAMSIQNMSEGGARAGMV 245
Db      174  LGAGVTSKQITMALIEKISAGATGYAIEFTGPALISALSYEARNTICNMVVERAGARAFM 233
Qy      246  APDETFEYELKGRPLAPKXYSPEWEKATQYWKMLQSDPGAKYDIDVFIIDAKDIPVTLTWG 305
Db      234  APDDKVFATLQHKRPAPK--GKLMEQAIDHWKTLHSDDEGAVFREVILDVAAELPEMTWG 291
Qy      306  TSPEDVVPITGVVPDEPTEPATEKKAQDGRMLQYMGKAGTPEMEDIPVDKVFISCTNSR 365
Db      292  TSPDOAAPRIKAVHPBPAPQDPDLTLRQGLRALDYMWLTTPGMPPLNEVTI SHAFIGSCTNAR 351
Qy      366  IEDLAAAVVYGRKKAPVKSAMVPGSGIVTQAEBESLDKIPBEGAGHEWREAGSGMC 425
Db      352  IEDLDVAAVVGRKVAHAHR-AMIVPGSTLVANQAEDBSLQIPLDAGFEMRSGSGSCMC 410
Qy      426  LGMNPDILAPOERCASSTNSRNEGROGAGARTHLMSPVMAAAAGIVGKLDVRLTDYKA 485
Db      411  LAMNDVLAIPGRCCASSSTNRNFEGRGAGARTHLMSPVMAAA--ISCHLIDVRIV----- 464
Qy      486  SPHIAAYQKSVITKPHVDERINODAEKDI IADI PEDNNGPHTNTSASVGTSAGLPKFTI 545
Db      465  -----ALEAXT-----I-----MCPEDT 476
Qy      546  LKGIAPLEKAWVDPAIIPKQFLKTIKRTGLGNALFYEMREFNEDGTEKSDPYLANKPEYR 605
Db      477  VSGSAPPLASINIDVIMPKQFLKGIQDQDLRGLFPDRLPLASGEPNPEFVLNQPAWQ 536
Qy      606  KASIIIVCTGANGCCSSSRHAPWALNDFGIRSVIAPSFADIFPNNSFKNMGLPIPIKQQA 665
Db      537  DAPFLV-TGPNNGCCSSSRHAWGLQVGRALIGTFPAGIFPDNCRNGVLAIQI--DDA 594
Qy      666  QI-----EALIAEAPAKIEIVDIPNQLKNATGETICTFEVEBFKXCLVNGLDIGLITM 721
Db      595  QKRVAAEATISVPATA--RISVNLACQTELELDG--TLIFEIFDQLRKQSLHGLDAIGTTL 651
Qy      722  QMEDKIAFEACHTRETPWLDGTGYLKRKQ 752
Db      652  QTEQIRAFEARHLADNPWL---GXWQKNGR 679

RESULT 22
PCT-US02-03987-5730
; Sequence 5730, Application PC/TUS0203987
; GENERAL INFORMATION:
; APPLICANT: Elitza Pharmaceuticals, Inc.
; TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits Ce
; TITLE OF INVENTION: Proliferation
; FILE REFERENCE: ELITRA.028VPC
; CURRENT APPLICATION NUMBER: PCT/US02/03987
; CURRENT FILING DATE: 2002-02-02
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 15811
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5730
; LENGTH: 644
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(644)

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OTHER INFORMATION: Xaa = Any Amino Acid
PCT-US02-03987-5730

Query Match 41.1%; Score 1666.5; DB 1; Length 644;
Best Local Similarity 48.7%; Pred. No. 7.8e-157;
Matches 352; Conservative 92; Mismatches 198; Indels 81; Gaps 10;

Qy 9 QTLVDKVLQAHVDEKLDGTLLYIDRLHVEHTVSQAFEGELNAGRKVRPPDCTLATTD 68
Db 3 QTLFDKVMNRHVLKGLPEQLLYIDLHLIHEVTSQAFEGELNQRKLRRPDLTFTATLD 62

Qy 69 HNVPTTSRKALKDIASFIEDDSRTQCVTLEENKVEFGVTFGLSDKRQGIYHVIGPEQG 128
Db 63 HNVPTI-----DIFN-IKDEIANKQITTLQKNAIDFGVHIFDMGSDDEQGIYHVMGPETG 115

Qy 129 FTLPGTTVCGDSHTSHGAFGALAGIGTSEVEHVLATQCLITKRSKNMRIQVGDGLAP 188
Db 116 LTPQKTIIVCGDSHTATHGAFGAIAFGIGTSEVEHVFATQTLWQTKPNKLDINGTLPT 175

Qy 189 GVSSKDVVLHAIGIIGTAGGTGAVIEFCGVSIRLSMEARMSICNMSTEGGARAGVAPD 248
Db 176 GYAKDIIHLIKTYGVDFGTGVALEFGETIKLSMDGRMTICNNAIEGGAKYGIQPD 235

Qy 249 EITFEYLKGRPLAPKYDSPWHKATQYWKNLQSDPGAKYDIDVFIADKDIVPTLTWGTSP 308
Db 236 DITFEYVKGRRFPADNF-----AKSDVKWRELYSDDDAIFDVRVIELDVSTLEPQVWTGTP 290

Qy 309 EDVVPITGVVDPETFEATEAKKAGRRMLQYMGKAGTGMEDIIPVDKVFIGSCTNSRIED 368
Db 291 EMGVNFSEPPF-----EISDINDQRAYDMGLEPFGQKAEIDILGYVFLGSCTNARLSD 343

Qy 369 LRAAAVVKGRKKAPNVKSNMVPVPGSLVKTOAEELGDKIFEEAGFEWREAGCSMCLGM 428
Db 344 LIEASHIVKGNKVHPNI-TAIVVPGSRTVKREAEKGLDITFKNAGFEWREPGCSMCLGM 402

Qy 429 NPDIILAPQBRCASTSNRNFEGRQAGGRTHLMSFWMAAAAGIVGKLADVRKLTIDYKASPH 488
Db 403 NPQOVPEGVHCASSTSNRNFEGRQKAGTHLVSPAMAAAAAHGKFVDVRKV-----454

Qy 489 IAAVQKSTVTKPHVDERINQDAHEKDIADI PEDNNGPHTNTSASVGTSGAGLPKFTILKG 548
Db 455 -----VYXMAAIKPIITYKG 469

Qy 549 IAAPLEKANVDTDAIIPKQFLKTIKRTGLGNALFYEMRFNEDGTEKSDFFVLNKEPYRKAS 608
Db 470 KIVPLFNDNIDTQIIPKVHLKRIKSGSGFPFAFDEWRYLPDGSNDPFPNPKPYKKGAS 529

Qy 609 ILVCTGANFGCGSSRSHAPWALNDFGIRSVIAPSPADIFNNFKNGMLPIPIKDAQIIE 668
Db 530 ILI-TGDNFGCGSSRSHAAWALKDYGFHIIAGSFSDIFYMNCTKNAMLPVILEKNAR-E 587

Qy 669 ATAABEARKKELEVDLPNOLIKNATGETICTFEVEFRKHCLVGLDIDIGLTMQMEDKIA 728
Db 588 HIAKYV-----EIEVDLPNQTV--SSPKSPHFEIDETWKNKLVNGLDDIAILTQYESLIE 641

Qy 729 EPE 731
Db 642 KVE 644

RESULT 23
US-09-815-242-5730
; Sequence 5730, Application US/09815242
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Cart, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in

TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5730
; LENGTH: 644
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(644)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-815-242-5730

Query Match 41.1%; Score 1666.5; DB 22; Length 644;
Best Local Similarity 48.7%; Pred. No. 7.8e-157;
Matches 352; Conservative 92; Mismatches 198; Indels 81; Gaps 10;

Qy 9 QTLVDKVLQAHVDEKLDGTLLYIDRLHVEHTVSQAFEGELNAGRKVRPPDCTLATTD 68
Db 3 QTLFDKVMNRHVLKGLPEQLLYIDLHLIHEVTSQAFEGELNQRKLRRPDLTFTATLD 62

Qy 69 HNVPTTSRKALKDIASFIEDDSRTQCVTLEENKVEFGVTFGLSDKRQGIYHVIGPEQG 128
Db 63 HNVPTI-----DIFN-IKDEIANKQITTLQKNAIDFGVHIFDMGSDDEQGIYHVMGPETG 115

Qy 129 FTLPGTTVCGDSHTSHGAFGALAGIGTSEVEHVLATQCLITKRSKNMRIQVGDGLAP 188
Db 116 LTPQKTIIVCGDSHTATHGAFGAIAFGIGTSEVEHVFATQTLWQTKPNKLDINGTLPT 175

Qy 189 GVSSKDVVLHAIGIIGTAGGTGAVIEFCGVSIRLSMEARMSICNMSTEGGARAGVAPD 248
Db 176 GYAKDIIHLIKTYGVDFGTGVALEFGETIKLSMDGRMTICNNAIEGGAKYGIQPD 235

Qy 249 EITFEYLKGRPLAPKYDSPWHKATQYWKNLQSDPGAKYDIDVFIADKDIVPTLTWGTSP 308
Db 236 DITFEYVKGRRFPADNF-----AKSDVKWRELYSDDDAIFDVRVIELDVSTLEPQVWTGTP 290

Qy 309 EDVVPITGVVDPETFEATEAKKAGRRMLQYMGKAGTGMEDIIPVDKVFIGSCTNSRIED 368
Db 291 EMGVNFSEPPF-----EISDINDQRAYDMGLEPFGQKAEIDILGYVFLGSCTNARLSD 343

Qy 369 LRAAAVVKGRKKAPNVKSNMVPVPGSLVKTOAEELGDKIFEEAGFEWREAGCSMCLGM 428
Db 344 LIEASHIVKGNKVHPNI-TAIVVPGSRTVKREAEKGLDITFKNAGFEWREPGCSMCLGM 402

Qy 429 NPDIILAPQBRCASTSNRNFEGRQAGGRTHLMSFWMAAAAGIVGKLADVRKLTIDYKASPH 488
Db 403 NPQOVPEGVHCASSTSNRNFEGRQKAGTHLVSPAMAAAAAHGKFVDVRKV-----454

Qy 489 IAAVQKSTVTKPHVDERINQDAHEKDIADI PEDNNGPHTNTSASVGTSGAGLPKFTILKG 548
Db 455 -----VYXMAAIKPIITYKG 469

Qy 549 IAAPLEKANVDTDAIIPKQFLKTIKRTGLGNALFYEMRFNEDGTEKSDFFVLNKEPYRKAS 608
Db 470 KIVPLFNDNIDTQIIPKVHLKRIKSGSGFPFAFDEWRYLPDGSNDPFPNPKPYKKGAS 529

Db 116 LTQPGKTIIVCGDSHTATHGAFGAIAFGIGTSEVHVHVFATQTLWQTKPNLKDINGTLPT 175
QY 189 GVSSKDVVLHAIGIITAGTGTGAVIEFCGVSIRLSMEARMSICNNMSIEGGARAGMVAPD 248
Db 176 GUYAKDIIHLIKTKYGVDFGTGYALEFTGETIXNLSMDGRMTICNWAIEGGAKYGIQPD 235
QY 249 EITFEYLKGRPLAPKYDSEPHKATQYWNLOSDDPGAKYDIDVIDAKDIDVPLTWGTSP 308
Db 236 DITFEYVVKGRPPADNF-----AKSVKWRRELYSDDDAIFDRVIELDVSTLEPQVWTGPN 290
QY 309 EDVVPITGVVPPPEFATKAKADGRMLQYWGCLKAGTMEIDIPVDKVFIFGSCNRSIED 368
Db 291 EMGVNFSEFP-----EISDINDQRAYDYMGLEPGQKAEDIDLGVFIFGSCNARLSD 343
QY 369 LRAAAVVKGRKAPNVKSAMVVPVPGSLVKTOAEEBGLDKIFEEAGFEWREAGCSMCLGM 428
Db 344 LIEASHIVKGNKVHPI-TAIVVPGSRTVKREAELGLDTIFKNAGFEWREPGCSMCLGM 402
QY 429 NPDILAPQERCASTSNRNFEGRQAGRTHLMSPVMAAAGIVGKLADVRKLTIDYKASPH 488
Db 403 NFDQVPEGVHCASSTSNRNFEGRQAGRTHLVSPMAAIIHGKFVDVRKV----- 454
QY 489 IAAVOKSVTKPHVDERINQDAHEKDIIADIPEDNNGPHNTSASVCTSAGLPKFTILKG 548
Db 455 -----VXXMAAIKPIITYKG 469
QY 549 IAAPLEKANVDTDAILPKQFLKTIKRTGLGNALFYEMRFNEDGTEKSDFVLNKEPYRKAS 608
Db 470 KIVPLFNDNIDTDQIIPKVHLKRISKSGPGFPAFDEWRYLPDGSNDPDPFNPKNKPYKAS 529
QY 609 ILVCTGANFGCGSSREHAPWALNDFGIRSVIAPSFADIPFNNSFKNGMLPIPIKDOAQIE 668
Db 530 ILI-TGDNFGCGSSREHAAWALKDYGFHIIAGSFSDIFYMNCTKNAMLPIVLEKNAR-E 587
QY 669 AIAAEARAGKEIEVDLPNQLIKNATGETICTPEVEERKHCLVNGLDDIGLTMQMEDKIA 728
Db 588 HLAKEY-----EIEVDLPNQTV--SSPDKSGFHEIDETWKNKLVNGLDDIAITLOYESLIE 641
QY 729 EFE 731
Db 642 KYE 644

Search completed: March 17, 2003, 08:53:54
Job time : 169 secs